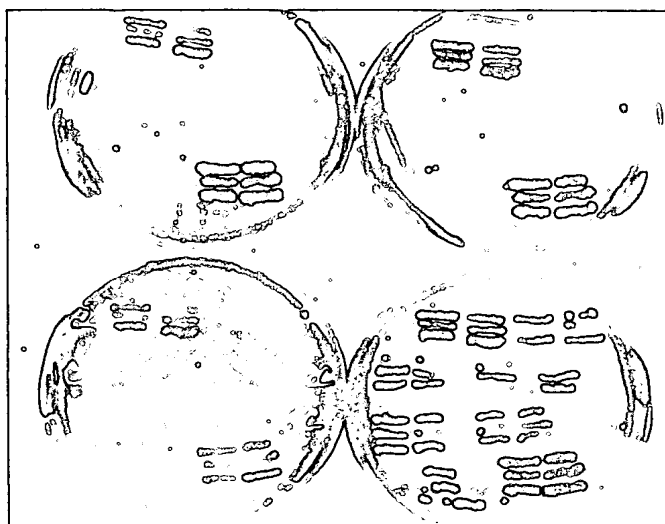


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SC galactose, 100 mM KCl

SC glucose, 0mM KCl

SC galactose, 0 mM KCl

SC glucose, 100 mM KCl

FIG. 1

330	Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ala Pro Ile Pro Ser Arg	350
	TAC ACA CTG CCA CGT TCC AAT TCG TCC GAT CCG GAT CTG AGC ATG TAC TAC CGC GTG GAG CCG GCT CCC ATT CCC AGC CGG	
	Lys Arg Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly Met Val His Ala Asn Ser Asp	1125
	AAG AGG GCA TTC TCC GTG TGC GCC GAC ATG GTT GGC GCC CAA AGG GAG GCG GGC ATG GTA CAC GCC AAT TCC GAT	400
380	Thr Asp Leu Thr Lys Leu Asp Arg Glu Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu	1200
	ACG GAT CTA ACC AAA CTG GAT CGC GAG AAG ACA TTC GAG ACG GCG GAG GCG TAC CAC CAG ACC ACC GAT TTG CTG	
	Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Ala Glu Gln Glu Asp Ala Ala Leu Tyr Gly Gly	1275
	GCC AAG GTG GTC AAC GCA CTG GCC GAC GCG GTG AAG CCA CCG CCG GCG GAA CAG GAA GAT GCG GCT CTC TAT GGT GGC	450
430	Tyr His Gly Phe Ser Asp Ser Gln Ile Leu Ala Ser Glu Thr Trp Ser Phe Ser Thr Val Asn Glu Phe Thr Ser Pro	1350
	TAT CAT GGC TTC TCC GAC TCC CAG ATC CTG GCC GCG GAA TGG TCG TTC TCG ACG GTC AAC GAG TTC ACA TCA CCG	
	Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg	1425
	CGA CGT CCA AGA GCA CGT GCC TGC TGC TCC GAT TTC AAT CTG GAG GCA CCT CGC TGG CAG AGC GAG AGG CCA CTG CGT	500
480	Ser Ser His Asn Glu Thr Thr Trp Ser Gly Asp Asn Gln Ile Gln Glu Ala Phe Asn Gln Arg Tyr Lys Gly	1500
	TCG AGC CAC AAC GAA TGG ACA TGG AGC GGC GGC GAC AAC CAG CAG ATC CAG GAG GCA TTC AAC CAG CGC TAC AAG GGA	
	Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met Val His Leu Glu Pro Asp Ala Leu Glu Gln Leu Arg	1575
	CAG CAG CGT GCC AAC GCA GCC AAC TCG ACC ATG GTC CAT CTG GAG CCG GAT GCT TTG GAG GAG CAG CTG AGA	550
530	Asn Asn His Arg Val Pro Val Ala Ser Arg Ser Pro Cys Arg Met Val Cys Asp Val Cys Phe Pro Ser Arg	1650
	AAC AAT CAC CCG GTG CCG GTC CCG TCA AGA AGT TCT CCA TGC CGG ATG GTC TGC GAC GTC GTC TGT TTC CCT TCC AGA	
	Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys	1725
	AGA AGC ACC CCT CGC AGG ATC TGG AGC GCA AGT TGT CCG TGG TCT CGG TAC CCG AGG GTG TCA TCT CGC AGG AAG	600
580	Pro Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Pro Pro Val Asn Pro Ile Cys Ala Thr Asp Ala	1800
	CCA GAT CCC CGC TGG ACT ACT ACA TCA ACA CGG TCA CCG CGG CCT CCA GTC AAT CCT ATT TGC GCA ACG GAC GCG	
	Val Arg His Arg Pro Ser Asn Arg Met Ala Ala Trp Pro Ala Ala Gly	1880
	GTC CGC CAC CGC CCT TCG AAT CGA ATG GCA GCT TGG CCA CCG GCG GCG GGC TAA CGAACATGGGCTTCCAGATTGGAG	
	GATGGAGCAACCCGCCATCGGCATTGGCGGTGGAGCCCTATCAACGCAAGCGCGTGTGGCAAGCGCCGACGCGAGAGCATCTACACCCAGAATCAA	
	GCCCCATCCGTCGCCGGGCAGCATGTATCCGCCGACCGCGACCGCTTGGCCCGAGATGCAGATCGACGCGGAGGTGGCAACCCAGTGGCTCTGGA	
	TCGGCGGCCATGGCGCAGTGGCGCGTGGCAGCCTCTTCCAGCTACAGCATCGGCATCATCGCTGACCTTGGTTCGCGGCCGGAAGCAGCATA	
	TTCTCGGTTACCTCCGAAAAGGATATGAATGTGCTGGAGCAGACCAATTCGCGGATCTGATTCGTGGCGCTCGAG . . . 3'	

3.

10 20
 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser Asn Glu Val Lys
 ATG TCC GAT CAG CTG TTT GTC GCA TTT GAG AAG TAT TTC TTG ACG AGT AAC GAG GTC AAG 60
 30 40
 Lys Asn Ala Ala thr Glu Thr Trp Thr Phe Ser Ser Ser Ile Phe Phe Ala Val Thr Val
 AAG AAT GCA GCA ACG GAG ACA TGG ACA TTT TCA TCG TCC ATT TTC TTT GCC GTA ACC GTC 120
 50 60
M5-1
 Val Thr Thr Ile Gly Tyr Gly Asn Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys
 GTC ACT ACC ATC GGA TAC GGT AAT CCA GTT CCA GTG ACA AAC AAT GGA CCG ATA TGG TGT 180
 70 80
 Ile Leu Phe Ser Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
 ATA TTG TTC TCC TTG CTT GGA ATA CCT CTA ACA CTG GTT ACC ATC GCT GAC TTG GCA GGT 240
 90 100
 Lys Phe Leu Ser Glu His Leu Val Trp Trp Leu Tyr Gly Asn Tyr Leu Lys Leu Tyr Leu
 AAA TTC CTA TCT GAA CAT CTT GTT TGG TTG TAT GGA AAC TAT TTG AAA TTA AAA TAT CTC 300
 110 120
 Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His Val Cys Glu His Cys His Ser His
 ATA TTG TCA CGA CAT CGA AAA GAA CGG AGA GAG CAC GGT TGT GAG CAC TGT CAC AGT CAT 360
 130 140
 Gly Met Gly His Asp Met Asn Ile Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala
 GGA ATG GGG CAT GAT ATG AAT ATC GAG GAG AAA AGA ATT CCT GCA TTC CTG GTA TTA GCT 420
 150 160
M3
 Ile Leu Ile Val Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
 ATT CTG ATA GTA TAT ACA GCG TTT GGC GGT GTC CTA ATG TCA AAA TTA GAG CCG TGG TCT 480

FIG. 3A

170 H5-2 180
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly Phe Gly Asp Leu
TTC TTC ACT TCA TTC TAC TGG TCC TTC ATT ACA ATG ACT ACT GTC GGG TTT GGC GAC TTG 540
190
Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu Tyr Ile Ile Leu Gly Lys Phe
ATG CCC AGA AGG GAC GAC TAC ATG TAT ATC ATA TTG CTC TAT ATC ATT TTA GGT AAA TTT 600
210 M4 220
Ser Met Lys Lys Lys Lys Phe Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys
TCA ATG AAA AAA AAA CAA AAA TTT TTA GGT CTT GCA ATA ACT ACA ATG TGC 660
230
Ile Asp Leu Val Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
ATT GAT TTG GTA GGA GTA CAG TAT ATT CGA AAG ATT CAT TAT TTC GGA AGA AAA ATT CAA 720
250
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val Ser Glu Leu Tyr
GAC GCT AGA TCT GCA TTG GCG GTT GTA GGA GGA AAG GTA GTC CTT GTA TCA GAA CTC TAC 780
270
Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser Arg Glu Ala Phe Ile Val Glu Asn
GCA AAT TTA ATG CAA AAG CGA GCT CGT AAC ATG TCC CGA GAA GCT TTT ATA GTG GAG AAT 840
290
Leu Tyr Val Ser Lys Lys His Ile Ile Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr
CTC TAT GTT TCC AAA CAC ATC ATA CCA TTC ATA CCA ACT GAT ATC CGA TGT ATT CGA TAT 900
310
Ile Asp Gln Thr Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln
ATT GAT CAA ACT GCC GAT GCT ACC ATT TCC ACG TCA TCG TCT GCA ATT GAT ATG CAA 960
330 336
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
AGT TGT AGA TTT TGT CAT TCA AGA TAT TCT CTC AAT CGT GCA TTC AAA TAG 1011

FIG. 3B

Ce orf1	-----	-----	-----	-----	-----	
Dm orf1	MSPNRWILL	IFYISYLMFG	AAIYYHIEHG	E EKISRAEQR	KAQIAINEYL	50
Consensus	50
Ce orf1	-----	--MSDQLFVA	FEKYFLTSNE	VKKNAATE	TFSSSIFFAV	38
Dm orf1	LEELGDKNTT	TQDEILQRI	DYCDKPVTL	PTYDDTPY	TFYHAF	100
Consensus	100
Ce orf1	TVVTTIGYGN	PVPMINIGRI	WCILFSLIGI	PLTLVTIADL	AGKFLSEHLV	88
Dm orf1	TVCSIMGYGN	ISPIITFAGRM	IMIAYSVIGI	PVNGILFACL	-----	140
Consensus	TV..T.GYGN	..P.T..GR.	..I..S..GI	P.....A..L	150
Ce orf1	WLYGNYLKLK	YLILSRHRKE	RREHVCEHCH	SHGMCHDMNI	E EKRIPAFLV	138
Dm orf1	---GEYFGRT	FEAIYRRYKK	YKMSTDMHYV	PPQLGLITTV	VIALIPGIAL	187
Consensus	...G.Y....R..K.H..S.....IP....	200
Ce orf1	LAILIVYTAF	GGVLMKLEP	WSFFTSEYWS	FITVTTMGFG	DLMPRRQGYM	188
Dm orf1	FLVLPCVGVH	LLRELGLSS-	----ISLYMS	YVITTTIGFG	DYVPT-FCAN	231
Consensus	...L.....S.Y.S..	T.TT.CFG	D...P...G..	250
Ce orf1	YIILLYIILG	KFSMKKKQKF	KIFLGLAITT	MCIDLVGVOY	IRKIHVFGRK	238
Dm orf1	QPKEFGGWV	VYQIFVIVWF	IFSLGYLVMI	MTFITRGLOS	KKLAYLEQQL	281
ConsensusF.....LG.....	M.....G..Q.	300
Ce orf1	IQDARSALAV	VGGKVLVSE	LYANLMQKRA	RNMSREAFIV	ENLYVSKHII	288
Dm orf1	SSNLKATQNR	IWSGVTKDVG	YLRRLNELY	ILKVKPVYTD	VDIAYTLPRS	331
ConsensusV.....	350
Ce orf1	PFITDIRCI	-RYIDQTADA	ATISTSSSAI	DMOSCRFCHS	RYSLNRAFKK	337
Dm orf1	NSCPDLSMYR	VEPAPIPSRK	RAFSVCADMV	GAOREAGMVH	ANSOTDLTKL	381
Consensus	...P.....S.....Q.....S.....K.	400
Ce orf1	-----	-----	-----	-----	-----	337
Dm orf1	DREKTFETAE	AYHQTTDLLA	KVVNALATVK	PPPAEQEDAA	LYGGYHGFS	431
Consensus	450
Ce orf1	-----	-----	-----	-----	-----	337
Dm orf1	SQILASEWSF	STVNEFTSPR	RPRARACSD	F NLEAPRWQSE	RPLRSSHNEW	481
Consensus	500

FIG. 4

034501.03449

mIRK	AFLFSIETQTTIGYGFRVCVTDECP	{G,A,S,T}, {D,E}
hROMK1	AFLFSLETQVTIGYGFRVTEQCA	{N,Q}, {K,R,H}
rGIRK1	AFLFFIETEATIGYGYRYITDHCP	{F,Y,W}={I,L,M,V}
Dm H5-1	
	AFFFAFTVCSTVGYGNISPTTFAG	
	. .	
Shak	AFWWAVVTMTTVGYGDMTPVGFVG	
Shal	AFWYTIVTMTTLGYGDMVPETIAG	
Shab	AFWWAGITMTTVGYGDICPTTALG	
Shaw	GLWWALVTMTTVGYGDMA PKTYIG	
Eag	ALYFTMTCMTSVGFGNVAAETDNE	
Slo	CVYFLIVTMSTVGYGDVYCETVLG	
Dm H5-2	. .	
	SLYTSYVTTTTIGFGDYVPTFGAN	
Dm H5-1	AFFFAFTVCSTVGYGNISPTTFAG	
Ce 5-1	SIFFAVTVTTTIGYG NPVPVTNTG	
Dm H5-2	SLYTSYVTTTTIGFGDYVPTFGAN	
Ce H5-2	SFYWSFITMTTVGF GDLMPRRDGY	

FIG. 5A

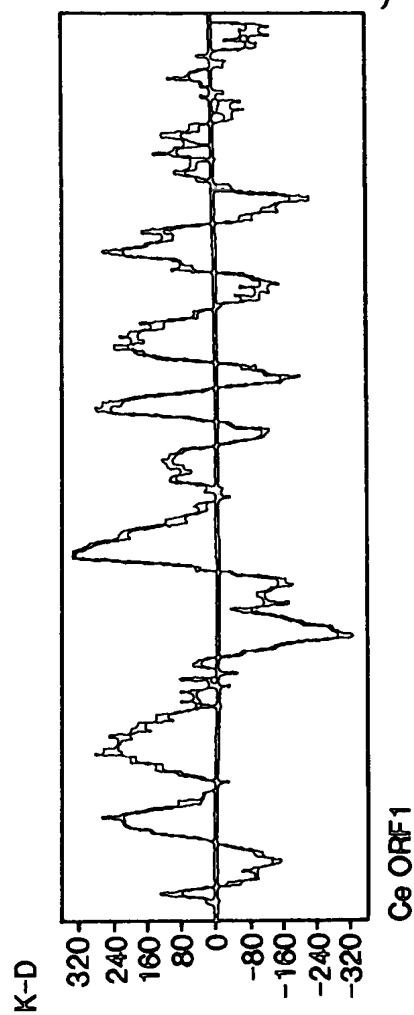
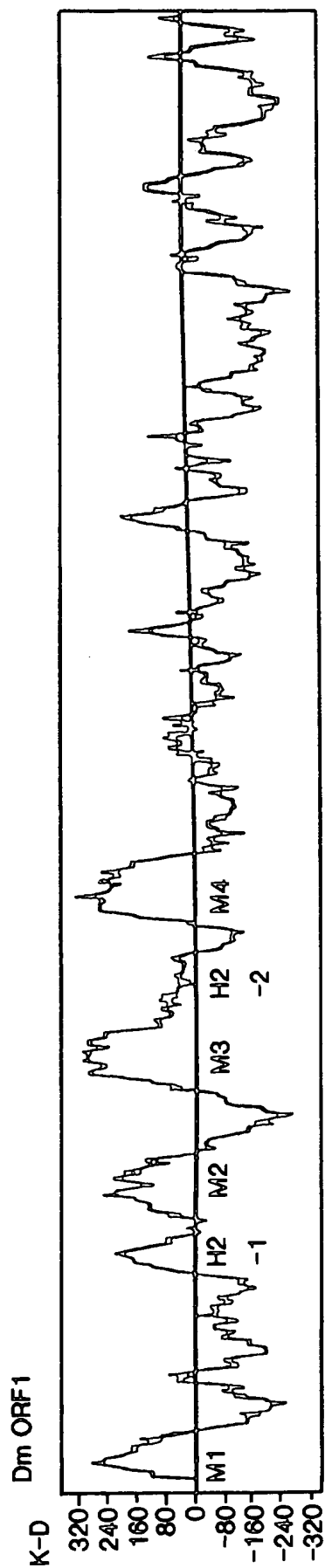
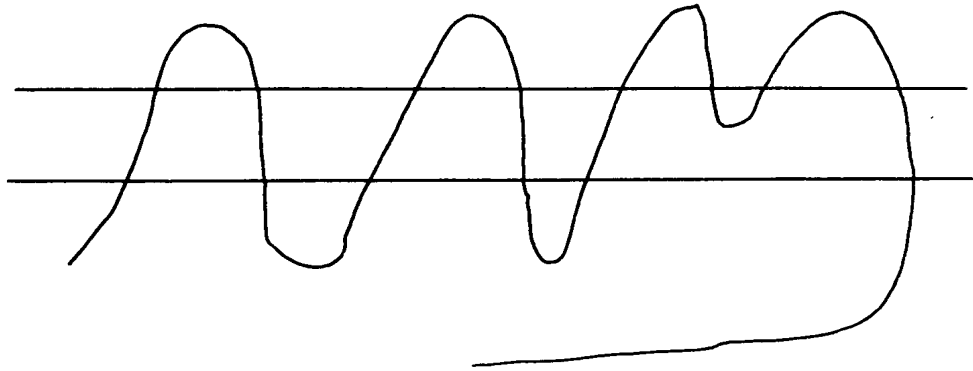


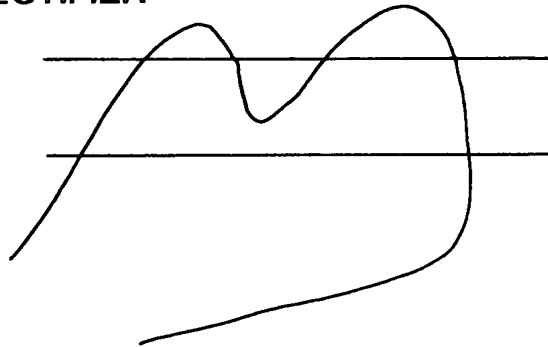
FIG. 5B

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46T20" T09T880

1) SHAKER



2) INWARD RECTIFIER



3) ORF1

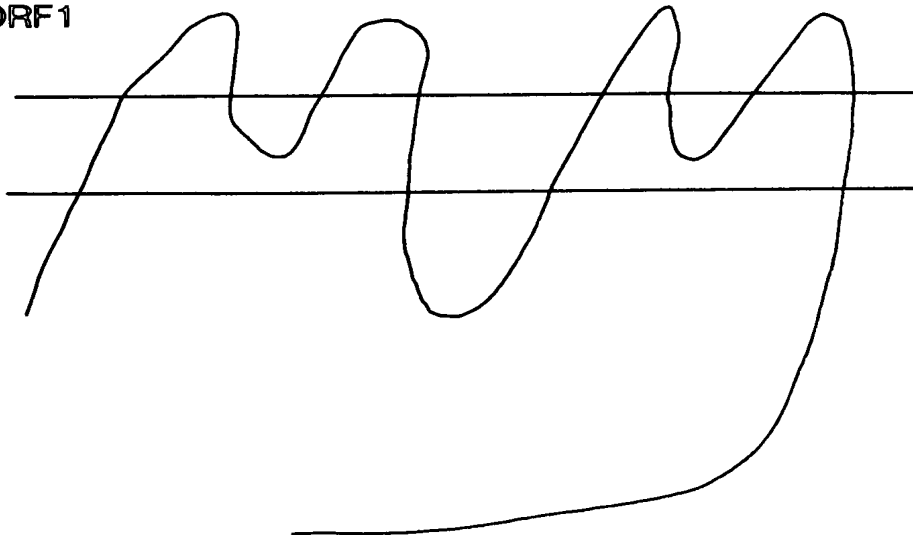


FIG. 6

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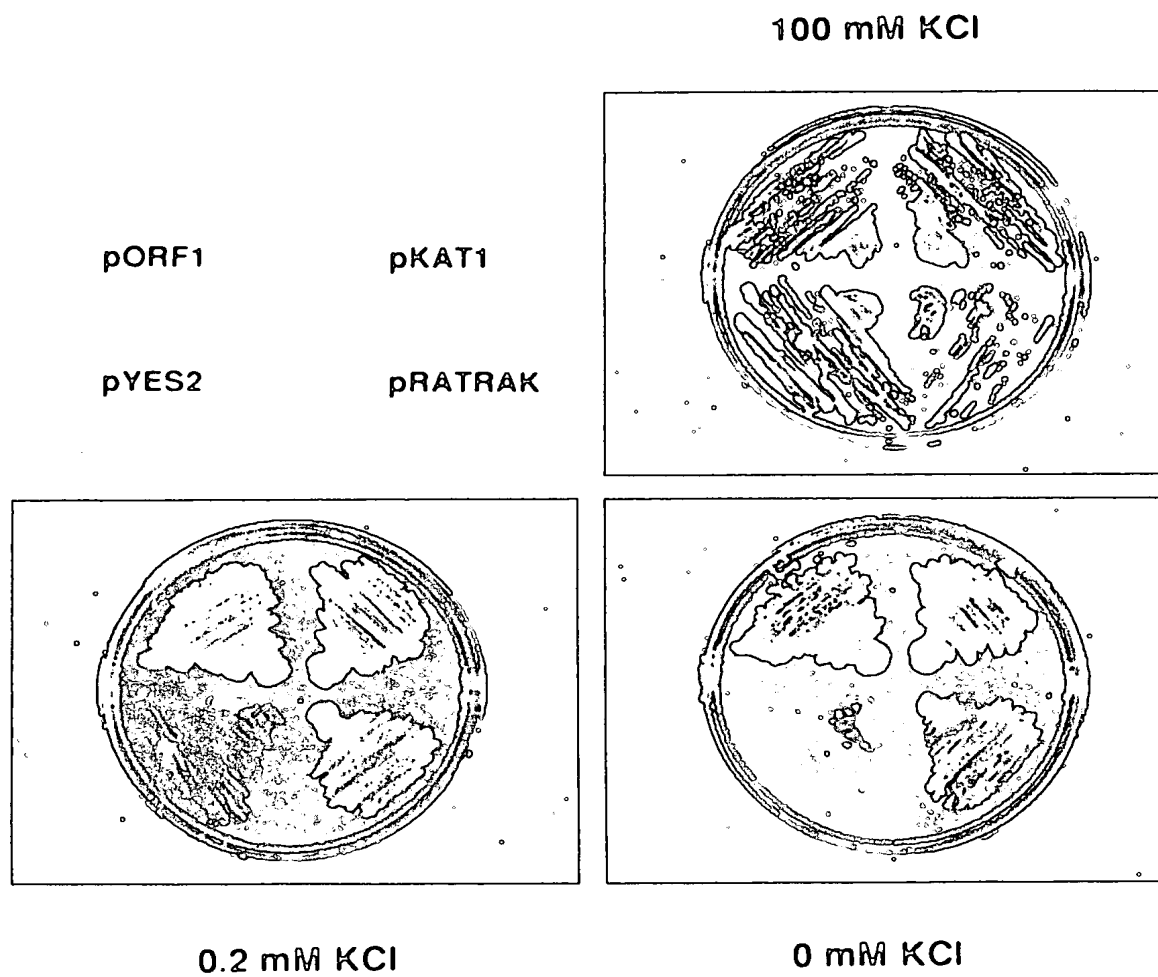
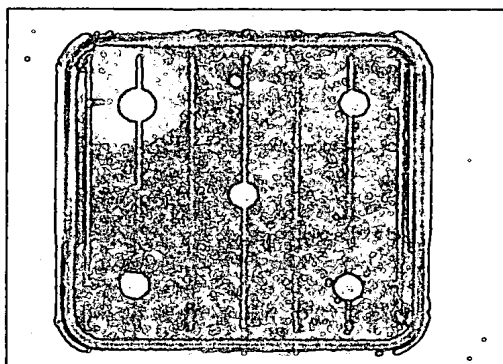


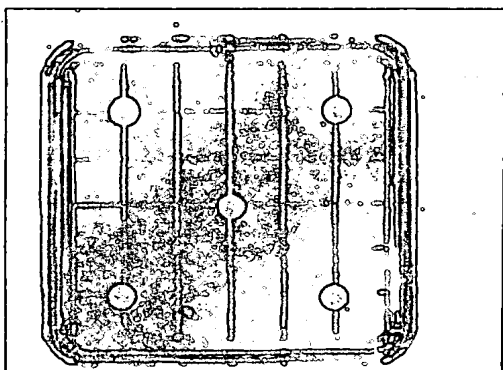
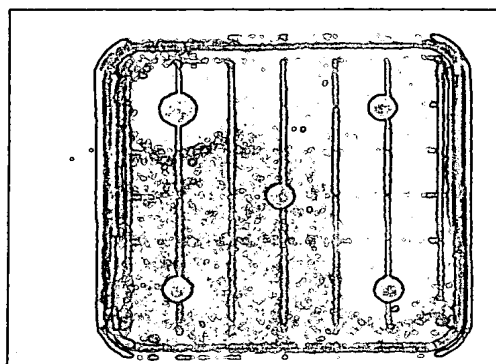
FIG. 7

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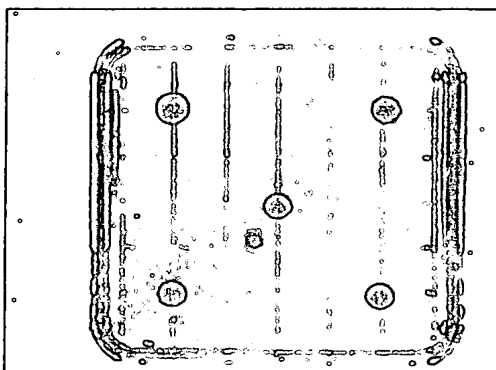
pORF1



pKAT1



pRATRAK



pYES2

FIG. 8

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala Phe Pro Arg Asp Lys Tyr Asn Ile Val 20
 ATG GTA ATA ATC AAC CGA TCG AAC ACC TAT GCC GTT GAG CAG GAA GCA TTT CCA AGA GAC AAG TAC AAT ATT GTC 75

 Tyr Trp Leu Val Ile Leu Val Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro Glu Tyr 50
 TAC TGG CTC GTC ATT CTT GTT GGA TTC GGA GGT CTT CTG CCA TGG AAT ATG TTC ATT ACT ATC GCC CCT GAG TAT 150

 Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile 70
 TAT GTG AAT TAT TGG TTC AAA CCG GAT GGC GTG GAG ACA TGG TAT TCG AAA GAA TTC ATG GGT CCC CTG ATC TAC CGC 225

 Gly Ser Gln Leu Pro Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ala Gly Pro Leu Ile Tyr Arg 100
 GGC TCA CAA CTT CCA AAC GCA AGC ATT AAT GGT TTC AAC CTG TTC TCG AAC CTG TTT GCT GGT CCC CTG ATC TAC CGC 300

 Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Ile Val Thr Ile Leu Val Ile Val Leu Glu Pro Thr 120
 GTC TTT GCT CCG GTT TGC TTC AAC ATC GTC AAC CTG ACA ATC ATT CTC ATC CTC GTC ATT GTT CTG GAG CCC ACT 375

 Glu Asp Ser Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn Phe Ser Asn Gly Leu Tyr 150
 GAA GAT TCC ATG TCC TGG TTT TTC TGG GTA ACT CTT GGA ATG CCG ACT TCA ATC AAT TTT AGC AAT GGG CTA TAT 450

 Glu Asn Ser Val Tyr Gly Val Gly Asp Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile 170
 GAA AAC TCG GTT TAT GGA GTT GGT GGC GAT TTT CCG CAC ACC TAC ATT GGC GCT CTC TTG ATT GGA AAC AAC ATT 525

 Cys Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn Asp Glu Pro Lys Leu Val Ala Ile 200
 TGC GGA TTG CTG ATA ACG GTT GTG AAA ATC GGA GTG ACC TAT TTT CTG AAT GAT GAG CCT AAA CTT GTT GCA ATC 600

 Val Tyr Phe Gly Ile Ser Leu Val Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp Phe 220
 GTC TAT TTC GGC ATA TCG TTG GTG ATC CTT CTG GTG TGT GCA ATT GCA CTT TTC TTT ATC ACA AAG CAA GAT TTC 675

FIG. 9A

230 Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu 250
 TAC CAC TAT CAC CAT CAA AAA GGA ATG GAA ATT CGC GAA AAG GCG GAA ACC GAC AGA CCG TCT CCA TCC ATT CTT 750

 260 Trp Thr Thr Phe Thr Asn Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu Thr Ile Phe
 TGG ACC ACA TTC ACA ACC ACC GTT ACC ACT CGT GGA GAT TCC GGC TTC CTA AAC AAA ATT ATG TCT GAA AAC GAT GAA ATC 825

 280 Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile
 CCT GTT ATG ATG ACC ACC GTT ACC ACT CGT GGA GAT TCC GGC TTC CTA AAC AAA ATT ATG TCT GAA AAC GAT GAA ATC 900

 310 Tyr Thr Leu Leu Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ile Gly Ser Ile Val Ala Ser Lys Ile His
 TAC ACT TTG CTC ACA AGT TTC CTC GTC TTC AAT TTC GCG GAT TCC ATA GGT GCT TCC AAG ATT CAC 975

 330 Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Cys Asn
 TGG CCG ACA CCC CGT TAC CTC AAA TTT GCC ATA ATC TTC CGT GCT CTT TTC CCA TTC TTC TTC TCC TGC AAC 1050

 360 Tyr Arg Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Thr Asp Ile Phe Val Ile Gly Gly Ile Ala Met
 TAT CGT GTC CAG ACG CGT GCT TAT CCT GTT TTC TTT GAG TCT ACT ACT GAC ATT TTT GTG ATT GGT GGA ATT GCC ATG 1125

 380 Ser Phe Ser His Gly Tyr Leu Ser Ala Leu Ala Met Gly Tyr Thr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
 TCT TTT TCA CAT GGA TAC CTC AGC GCT CTG GCA ATG GGA TAC ACT CCA AAC GTC GTG CCA TCT CAC TAC TCA AGA 1200

 410 Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Thr Gly Gly Leu Trp Pro Val Val Ile Glu
 TTT GCC GCT CAG CTT TCC GTT TGC ACT CTT ATG GTT GGC CTT CTC ACC GGT GGC CTG TGG CCC GTT ATT GAG 1275

 430 His Phe Val Asp Lys Pro Ser Ile Leu
 CAC TTC GTG GAC AAG CCA AGT ATC TTA TAA ATATTATAGCATTAGAGTACTTGTATATGTTGTTTTTATTAAAGCTGGAATAAA 1364

 ATAAATTATAAAAAAAAAAAAA 1388

FIG. 9B

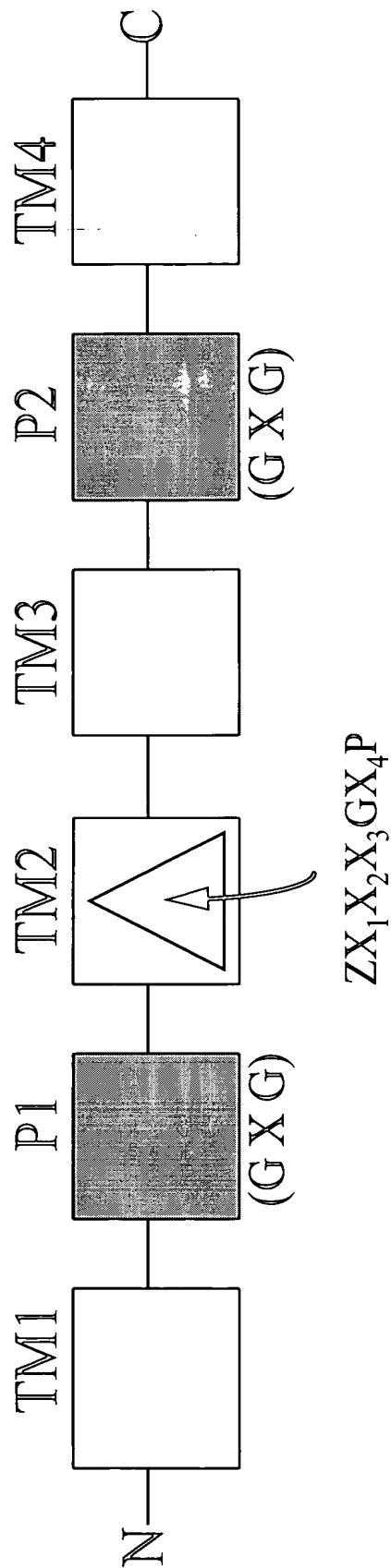


FIG. 10